

MBE Author-Subject Index
Volume 12

- A+C pressure, 558
 abalone sperm, 231
 ABELE, L. G., 291
Acanthamoeba, 533
 achaete, 382
 acquisitive evolution, 514
 actin-binding protein, 405
 ADACHI, J., 177, 782
 adaptive evolution, 53
 Africa, 334
 alcohol dehydrogenase gene, 391
 alignment, 980
 allelic variation, 582
 ALLENDORF, F. W., 1106
 α -amylase, 938
 α -amylase multigene family, 564
 ALTHEIDE, T. K., 902
 ALVES-GOMES, J., 298
 AMOS, B., 459
 ancestry, 980
 anchored restriction mapping, 103
 ANDERSON, W. W., 564, 938
 angiosperms, 1151
 Annelida, 641
Anopheles gambiae complex, 103
Anopheles gambiae, 850
 Anura, 928
 AP-PCR, 1022
Apis mellifera, 1074
 AQUADRO, C. F., 382
 ARBER, W., 198
 archaeobacteria, 1
 Aschelminthes, 1132
 Ascomycotina, 208
 Aves, 759
 AYALA, F. J., 616
- BACKELJAU, T., 641, 1132
 BAFNA, V., 239
 BAGUÑA, J., 421
 BALL, A. O., 735
 BARRIO, E., 616
 BAYASCAS, J. R., 421
 BEGUN, D., 382
 beluga, 582
 BERTORELLE, G., 887
 β -galactosidase, 514
 BEYNON, C. M., 521
 BHATTACHARYA, D., 415
 bias of G+C content, 782
 BIBEAU, C., 415
 bighorn sheep, 1106
 biochemical diversity, 1048
 biosynthesis, 834
 BLOT, M., 198
 body temperature, 834
- BOERWINKLE, E., 914
Bombus terrestris, 1074
 bootstrap, 319, 657, 814
 BOROWSKY, R. L., 1022
 BOURSOT, P., 334
 BOUSQUET, J., 1151
 BOYCE, T. M., 113
 BRIDGE, D., 679
 BRITTEN, R. J., 219
 BRONSON, D. L., 657
 BROOKS, J. M., 1132
 BUCHANAN, F. C., 1106
 BUGAJ-GAWEDA, B., 346
 bumble bee, 1074
 BURK, A., 1138
 BURKE, T., 459
 BURKE, W. D., 1094
 BURRESON, E. M., 573
 BUSS, L., 679
- Caenorhabditis*, 346
 CAINK, A. K., 83
 calcium-binding proteins, 967
 Caliciales, 208
 CAMPBELL, H. C., 405
 Carnivora, 690
 CASALI, A., 421
 CATZEFILS, F. M., 73
 Caudata, 928
 cave fishes, 527
Cavia porcellus, 168
 cetacean evolution, 518
 cetacean phylogeny, 177
 CHAKRABORTY, R., 914
 CHAMBERS, G. K., 28
 chaperones, 1048
 CHENG, R., 1022
 CHEVRET, P., 73
 chicken, 94
 chimpanzees, 594
Chlamydomonas, 533
 chloroplast DNA, 371, 533
 CHO, S., 650
 CHOI, E.-H., 748
 chromosomal evolution, 239
 Chrysomelidae, 627
Chrysoperla plorabunda, 850
 Cichlidae, 1033
 ciliates, 285
 circumsporozoite protein, 616
 CLARK, J. B., 902
 class II genes, 441
 CLAUDIANOS, C., 405
 clinal selection, 113
 clinal variation, 521
 clumping factor, 963

- Cnidaria, 679
 coalescent, 594
 codon usage, 219
 COLLINS, R. A., 7
 colony fusion, 494
 color vision, 53, 527
 combined approach, 627
 compatibility molecules, 494
 compensatory substitutions, 7, 1138
 competition, 1012
 composition, 359
 computer simulations, 7, 503
 concerted evolution, 481, 963
 concomitantly variable codons, 503
 concordance test, 650
 confidence sets, 291
 congruence analyses, 627
 constraints, 594
 control region sequences, 604
 copia, 83
 Coreopsis, 371
 CORNUET, J.-M., 1074
 COTE, V., 533
 CRAWFORD, A. M., 1106
 Crocodilia, 759
 CROZIER, R. H., 558
 CUMMINGS, M. P., 814
 CUNNINGHAM, C. W., 679
 cyanelle, 415
 cyanobacteria, 1166
Cyanophora paradoxa, 415
 cysteine, 708
 cytochrome b, 177, 518, 1114
 cytochrome oxidase III, 735

 DAVIDSON, E. H., 219
 DE BAERE, R., 671
 DE BOER, R. J., 494
 DEBRY, R., 291
 DEKA, R., 914
Delphinapterus leucas, 582
 departure from neutrality, 113
 DEPRIEST, P. T., 208
 DE RIJK, P., 671
 DESALLE, R., 679
 DE WACHTER, R., 641, 671, 1132, 1166
 dicot, 1151
 DILORIO, P. J., 1048
 dinucleotide repeats, 432
 directional nucleotide substitution, 1124
 directional selection, 959
 distance matrices, 266
 distances, 546
 divergence time, 1151
 divergence times, 391
 diversifying selection, 363
 DIXON, G. H., 708
 DNA, 814
 DNA evolution, 363
 DNA hybridization, 266
 DNA polymorphism, 382, 432
 DNA sequences, 451
 DÖRNER, M., 944
 DOWLING, H. G., 259
 DQB locus, 582
Drosophila, 83, 391, 902, 1002, 1094
Drosophila erecta, 62
Drosophila melanogaster, 180, 382, 723, 748, 959
Drosophila pseudoobscura, 564, 938
Drosophila simulans, 113
 Drosophilids, 823
 DROUIN, G., 481
Dugesia tigrina, 421
 DUNCAN, K. E., 1012

E. coli, 198, 514, 980
 EBG, 514
 Echiura, 641
 EICKBUSH, D. G., 1094
 EICKBUSH, T. H., 1094
 18S rDNA, 208
 18S ribosomal RNA, 346, 1132
 electrogenic and electrosensory systems, 298
 elongation factor 2, 782
 elongation factor-1 α , 650
 EM algorithm, 921
 EMMONS, S. W., 346
 endoplasmic reticulum, 1063
 endosymbiosis, 1166
 enhancer, 1002
 env gene, 803
 enzyme/crystallin, 773
 ESCALANTE, A. A., 616
 escape mutants, 803
 esterase 6, 113
 estimation of divergence time, 823
 ESTOUP, A., 1074
 Eukaryotes, 1, 782
 eutherians, 944
 even-skipped, 1002
 evolutionary model, 7
 evolutionary potential, 514
 evolutionary rate, 123
 evolutionary rates, 432, 503
 evolutionary trees, 863
 EXCOFFIER, L., 334, 921
 exon variation, 1157

 FANG, Y., 16
 FARAS, A. J., 657
 Felidae, 690
 FERGUSON, N., 1012
 FERNÁNDEZ, M.-P., 967
 FERRELL, R. E., 914
 fertilization—vertebrates, 231
 FIGUEROA, F., 1033
 finite-sites model, 887
 fish, 1048

- FITCH, D. H. A., 346
 FITCH, W. M., 198, 503
 FITZSIMMONS, N. N., 432
 5S ribosomal genes, 481
 flightless, 405
 FORBES, S. H., 1106
 FORS-D analysis, 1157
 FORSDYKE, D. R., 949, 1157
 FOSTER, T. J., 963
 founding, 1085
 four-cluster analysis, 163
Frankia, 16
 FREIMER, N. G., 594
 frequency dependent selection, 794
 frequency spectrum, 382
 FRIEDLANDER, T. P., 650
 FRYE, M. S., 168
 FU, Y-X., 546
 functional constraint, 123
 fungal mating-types, 794
 FUNK, D. J., 627
 FURANO, A. V., 73
 FUTUYMA, D. J., 627

 (G+C)/(A+T) ratio, 949
 G+C content, 451
 G+T pressure, 558
gag gene, 803
 GALINDO, M. I., 723
 gamete recognition, 231
 gamma distribution, 503, 546
 GARCIA-FERNANDEZ, J., 421
 GAREY, J. R., 1132
 GARGAS, A., 208
 GARZA, J. C., 594
 GAUT, B., 152
 gelsolin, 405
 gene arrangements, 564, 938
 gene conversion, 94, 247, 564, 938
 gene duplication, 1063
 gene evolution, 708, 967
 gene frequency estimation, 921
 gene rearrangement, 759
 gene regulation, 1002
 genetic distance, 914, 1106
 genetic drift, 1002
 genetic exchange, 1012
 genetic variability, 459, 473
 genome size, 834
 genomic mutation rate, 180
Giardia lamblia, 782
 Glaucocystophyta, 415
 GOLDING, G. B., 1
 GOLDSTEIN, D. B., 713
 GONZALEZ, P., 773
 gram-negative bacteria, 1
 gram-positive bacteria, 1
 GRAUR, D., 558
 GRAVEN, L., 334
 GRAY, M. W., 533
 great deluge algorithm, 863
 group I intron, 883
 group I introns, 208, 533
 GU, X., 546
 guinea pig, 773
 GUPTA, R. S., 1, 1063
 Gymnophiona, 928
gymnotiformes, 298

Hadamard transforms, 28
Haematobia irritans, 850
Haliotis sperm lysin, 231
 HALL, B. G., 514
Haplosporidium nelsoni, 573
 HARADA, K., 748
 HARTL, D. L., 62
 HASEGAWA, M., 177, 782
 HASHIMOTO, T., 782
 HAY, J. M., 928
 HAYGOOD, M., 298
 heat shock proteins, 1048
 HEDGES, S. B., 168, 259, 928
 HEILIGENBERG, W., 298
 HEISE, P. J., 259
 Heliethinae, 650
 HELMCHEN, T., 415
 HENDY, M. D., 863
Heterokonta, 671
 heteroplasmy, 893
 HICKSON, R. E., 28
 HIGHTOWER, L. E., 1048
 HILBISH, T. J., 893
 HIRSCH, A. M., 16
 histone, 481
 history of life, 1
 hitchhiking, 473, 959
 hitchhiking effects, 382
 HIV-1, 803
 HLA, 247
 hobo transposable element, 723
 HOGG, J. T., 1106
 HOLLAR, L., 1138
 HOLSINGER, K., 371, 988
 hominoid evolution, 823
 homology search, 949
Homo sapiens, 334, 863
 honey bee, 1074
 horizontal transfer, 219, 421, 850, 902,
 1094
 horizontal transmission, 62
 host-parasite, 616
 HOWELL, C. Y., 803
Hsp90, 1063
 HUELSENBECK, J. P., 843
 HUGHES, A., 247, 803
 HUGHES, M. K., 803
 human, 247
 human evolution, 334, 863, 887, 914
 humans, 594, 60
 hybrid dysgenesis, 723

- Hydrozoa, 679
Hyphochytrium, 671
Hyphochytrium catenoides, 671
- immunoglobulins, 94
 individuality, 494
 insect-plant interactions, 627
 insertion sequences, 198
 interchromosomal exchange of genetic information, 938
 interior-branch test, 319
 internal repeats, 967
 interrupted repeat sequences, 1074
 intraspecific variation, 371
 intron conservation, 1157
 intron mobility, 533
 introns early theory, 1157
 introns-early, 949
 In(2L), 748
 invariable sites, 546
 inversions, 239
IS630-Tc1 superfamily, 421
 ISTOCK, C. A., 1012
 IWABE, N., 123
- JANCZEWSKI, D. N., 690
 JANSEN, R. K., 371
 JERMIN, L. S., 558
 JIN, L., 914
- KALMES, R., 723
 KAMAISHI, T., 782
 KAROTAM, J., 113
 KIDWELL, M. G., 902
 KIRSCH, J. A. W., 266
 KLEIN, J., 1033
 KOCHER, T., 359
 KORNFELD, L., 1085
 KREITMAN, M., 1002
 KUMA, K.-I., 123
 KUMAR, S., 163, 1132
 KUMAZAWA, Y., 759
- LABEDAN, B., 980
 LADAVÈZE, V., 723
 LAMPE, D. J., 850
 LANGANEY, A., 334
 LAPOINTE, F.-J., 266
 large subunit rRNA gene, 533
 LAROCHE, J., 1151
 lateral transfer, 16
 LATHE III, W. C., 1094
 least squares distance, 713
 Lecanorales, 208
 LEE, Y.-H., 231
 LEMEUNIER, F., 723
 LEMIEUX, C., 533
 LEMKE, T. D., 657
 LENTO, G. M., 28
 Lepidoptera, 650
- leucine-rich-repeat, 405
 LEWIS, P., 152
 LI, M. D., 657
 LI, P., 1151
 LI, W.-H., 546
 LIAO, J., 16
 lichen-forming fungi, 208
 LIDHOLM, D.-A., 62
 life cycle evolution, 679
 likelihood ratio, 152
 LINE, 73
 LINE-1, 944
 linear invariants, 131
 linearized trees, 823
 linkage disequilibrium, 473, 794
 llama, 773
 LOHE, A. R., 62
 LI, 73
 LONERGAN, K. B., 533
 LUDWIG, M. Z., 1002
 LYNN, D. H., 285
 lysin, 231
- MACKEY, T. F. C., 180
 MACKEY, L. Y., 1132
 major histocompatibility complex, 441, 582
 major outer membrane protein, 363
 malaria, 616
 MALIK, S., 582
 mammalian evolution, 1138
 mammalian phylogeny, 944
 mammals, 168
 MARFANY, G., 421
 mariner, 421, 850
 mariner-like element (MLE), 62
 marine turtles, 432
 MARSHALL, C. R., 16
 marsupial, 441
 marsupial evolution, 708
 Marsupials, 266, 944
 MARTIN, A. P., 1114, 1124
 MASON, R. J., 371
 MATHIOPOULOS, K., 103
 MATZKE, E., 794
 maximum likelihood, 7, 152, 177, 291, 451, 546 814 843, 921
 MAXSON, L. R., 259, 928
 MAY, G., 794
 MAYER, W. E., 441, 1033
 mbuna, 1085
 McCLELLAND, M., 1022
 MCCUTCHAN, T., 103
 McDEVITT, D., 963
 McDONALD, J. F., 83
 MCGARVEY, S. T., 604
 MCKHANN, H. I., 16
 MEANY, A., 527
 medusa, 679
 MELKONIAN, M., 415

- MERCIER, J., 533
metabolic rate, 1124
 Metazoa, 558, 1132
 MEYER, A., 298, 518, 627
 MHC class I, 247
 microsatellite, 432, 473, 594, 914, 1074, 1106
 MILINKOVITCH, M. C., 518
Minchinia teredinis, 573
 minimum evolution tree, 163
 minisatellite evolution, 459
 minke whale, 459
missing data, 266
 MITCHELL, A., 650
 mitochondrial DNA, 103, 239, 298, 334, 359, 521, 533, 558, 604, 690, 759, 863, 893, 1114, 1124, 1151
 mitochondrial DNA inheritance, 735
 mitochondrial genome, 814
 mitochondrial 12S ribosomal RNA genes, 1138
 mitochondrion-lacking protozoa, 782
 MITTER, C., 650
 MIYAMOTO, M. M., 503
 MIYATA, T., 123
 mobile DNA, 902
 models, 451
 MODI, W. S., 690
 molecular, 168, 1132
 molecular clock, 391, 823, 1151
 molecular phylogenetics, 518, 650
 molecular phylogenies, 103, 346, 641, 967
 molecular sequence alignment, 967
 molecular systematics, 451, 928
 Mollusca, 893
 MONIZ DE SA, M., 481
 monocot, 1151
Monodon monoceros, 582
 MOORE, S. S., 432
 MORAN, P., 1085
 MORGAN, R. O., 967
 MORITZ, C., 432
 MORIYAMA, E. N., 62
 mtDNA, 1085
 mtDNA sequences, 627
 multilocus genotype, 921
 multiple enzymes, 980
 MUÑOZ-MÁRMOL, A. M., 421
 MURRAY, B. W., 582
 mutational processes, 1074
Mytilus, 521, 735, 893
 NAAS, T., 198
 NAKAMURA, F., 782
 NAKAMURA, Y., 782
 naphthalene-degradation, 1012
narwhal, 582
 NEI, M., 94, 131, 163, 319, 391, 719, 823
neighbor joining, 7, 319, 814, 843
Neisseria gonorrhoeae, 363
Neisseria meningitidis, 363
 NELISSEN, B., 1166
 Nemertea, 641
neutral mutations, 473
nifH, 16
nifK, 16
 9 b.p. deletion, 604
 NISHIDA, H., 883
 NISHIDA, M., 759
 nonfunctionalization, 527
 nonsynonymous substitution, 231
 NORRIS, C. E., 1048
nucleotide composition, 558
 nucleotide polymorphism, 113
nucleotide sequence data, 291
 nucleotide substitution, 546
 nucleotide substitution models, 131
 nucleotide substitution patterns, 627
 NUÑEZ, S. B., 773
 NUZHDI, S., 180
 OAKESHOTT, J. G., 113
 O'BRIEN, S. J., 690
ocular lens, 773
 OKAMOTO, K.-I., 782
one-parameter model, 503
 Ophryoglenina, 285
 optimality model, 834
 organic evolution, 834
 ORTI, G., 298, 518, 627
 OTA, T., 94, 231
 OTIS, C., 533
 OTTO, S. P., 814
 outgroup, 177
Out-of-Africa hypothesis, 863
 overdominance, 473
 Ovis, 1106
 PÄÄBO, S., 944
paralogous, 980
 parasite, 573
parasites, 494
 parsimony, 285, 291, 573, 814
 PASCUAL, L., 723
 PASSARINO, G., 334
Pellioiditis, 346
Pelodera, 346
 PENNY, D., 28, 863
 PERIQUET, G., 723
 PERNA, N., 359
 PEVZNER, P. A., 239
 phospholipase A2, 1157
phylogenetic analysis, 7
 phylogenetic inference, 163, 291, 319, 1114
phylogenetic methods, 1063
 phylogenetic reconstruction, 266, 657
phylogenetics, 405, 713, 814
 phylogenetic trees, 823
phylogenies, 1
 phylogeny, 53, 73, 152, 168, 239, 259, 298,

- 391, 415, 627, 690, 735, 759, 928, 988,
1022, 1033, 1132
pinnipedia, 28
planarian, 421
Planigales, 708
plasmid, 1012
Plasmodium species, 616
plastids, 1166
Pogonophora, 641
pol gene, 803
POLLOCK, D. C., 713
pol nucleotide and RT amino acid
sequences, 657
polymerase chain reaction, 759
polymorphism, 363
polymorphisms, 494
POOLE, R. W., 650
POPADIC, A., 564, 938
POPADIC, D., 938
population bottleneck, 1085
population genetics, 334 432, 459
population growth, 887
porB, 363
positive Darwinian selection, 363
positive selection, 803
POWELL, J., 103
promoter evolution, 773
promoter function, 773
protamine, 708
protein phylogeny, 782, 1063
protist phylogeny, 285
Protista, 573
Protomyces inouyei, 883
protozoan phylogeny, 616
pseudocoelom, 1132
pseudogenes, 94, 247
Pseudomonas putida, 1012

QUESADA, H., 521

RAO, P. V., 773
RAPD, 1022, 1033
Ras, 405
rate variation, 988
rate variation among sites, 546
ratites, 163
RAWSON, P. D., 893
rDNA, 481, 679
rearrangement, 239
recombination, 794, 949, 1157
recruitment of crystallins, 773
REDD, A. J., 604
REDDY, A., 16
red-necked wallaby, 441
REES, J. S., 708
REGIER, J. C., 650
relative-rate test, 1151
repeated DNA, 73
Reptilia, 259, 759
restriction site, 371
RETIEF, J. D., 708

retroelements, 657
retrotransposon, 73, 83, 219
retrotransposons, 748
reverse transcriptase, 219, 1094
RFLP, 198
Rhabditella, 346
Rhabditidae, 346
Rhabditis, 346
ribosomal DNA, 103
ribosomal DNA evolution, 208
ribosomal RNA, 641
ribosomal RNA genes, 928, 1094
RILEY, M., 980
RNA evolution, 7
ROBERTS, D., 451
ROBERTSON, H. M., 850
robustness, 843
rodent, 73
R1, 1094
rRNA, 988
rRNA phylogeny, 671
RUSSO, C. A. M., 391
RUVINSKY, I., 928
RZHETSKY, A., 131, 163, 319, 823

SAAVEDRA, C., 735
SALO, E., 421
SANTACHIARA-BENERECETTI, S., 334
Scaptodrosophila, 391
SCAPTOMYZA, 391
SCHLOSSER, M. J., 902
SCHULTZ, R. J., 1048
secondary intergradation, 521
secondary structure, 1138
SEIBERT, S. A., 803
selection, 1002
self-incompatibility, 794
self recognition, 494
SEMINO, O., 334
sequence alignment, 679
sequence comparison, 980
sequence evolution, 503
sequence-related families, 980
serpentes, 259
sharks, 1114
SHERRY, S. T., 604
SHIELDS, D. C., 963
short tandem repeats, 914
SHRIVER, M. D., 914
SIDDALL, M. E., 573
sigmodontine rodents, 988
SIMON, C., 988
simulation, 843
simulation study, 266
SINES, 481
single copy nuclear DNA, 103
Sipuncula, 641
site-specific endonuclease, 533
SITNIKOVA, T., 319
16S-like rRNA, 573
16S ribosomal RNA, 1166

- 16S rRNA, 298
 16S rRNA phylogeny, 16
 size homoplasy, 1074
 SKIBINSKI, D. O. F., 521
 SLADE, R. W., 441
 SLATKIN, M., 473, 594, 887, 921
 small subunit ribosomal RNA, 415
 SMITH, J. M., 363
 SMITH, N. H., 363
 snake venom, 1157
 SOFRO, A. S. M., 604
 soil microcosm, 1012
 SOLIGNAC, M., 1074
 Sophophora, 902
 South American electric fish, 298
 speciation, 231, 949
 species flock, 1085
 spectral analysis, 28
 sperm, 708
 sperm chromatin, 708
 sperm whale, 518
 sperm-egg interaction, 231
 SPRATT, B. G., 363
 SPRINGER, M. S., 219, 1138
 STANWOOD, R. R., 735
Staphylococcus aureus, 963
 stationarity of base composition, 131
 stationary phase, 198
 statistical tests, 7
 STEEL, M., 863
 stem-loop, 949
 STEPHAN, W., 959
 STEPHENS, J. C., 690
 STEWART, D., 735
 stochastic loss, 62
 STOKES, N. A., 573
 STONEKING, M., 604
 strand-specific directional mutation pressure, 558
 subfamily classification, 967
 substitution, 359
 substitution model, 152
 substitution rate, 1151
 SUGIYAMA, J., 883
 SUH, D-S., 748
 SULLIVAN, J., 988
 SÜLTSMANN, H., 1033
 supergene family, 123
 superoxide dismutase, 503
 suppressor of forked, 382
 systematics, 168, 679

 TAILLIEZ, C., 1074
 TAKEZAKI, N., 391, 604, 823
 tandem array, 963
 tandem repeated DNA, 914
 taxonomy, 73
 TAYLOR, J. W., 208
Teratorhadtis, 346
 test statistics, 131
 Testudines, 432

 thermotolerance, 1048
 TICHY, H., 1033
 TILLIER, E. R. M., 7
 tissue-specific expression, 123
 total evidence, 627
 transcription, 1002
 transfection, 723
 transitions, 713, 1138
 transposable element, 62, 421
 transposable elements, 180, 902, 1094
 transposition rate, 180
 transposition rates, 748
 transposon, 850
 trans-spliced leader, 481
 transversions, 713, 1138
 tRNA, 759
 TURMEL, M., 533
 TUSNEEM, N., 219
 12S and 16S ribosomal RNA, 259
 12S rRNA, 298

 unequal base frequencies, 451
 USDIN, K., 73

 VACQUIER, V. D., 231
 VAN DEN BROECK, I., 671
 VAN DE PEER, Y., 671, 1166
 VAN DER AUWERA, G., 671
 VAN PIJLEN, I. A., 459
 variable region genes, 94
 variation, 83, 794
 VERONA, R., 73
 vertical descent, 16
 Vestimentifera, 641

 WADDELL, P. J., 863
 WAKELEY, J., 814
 weighted evolutionary distance, 713
 weighted parsimony, 627
 WELSH, J., 1022
 WESTERMAN, M., 708
 WHITE, B. N., 582
 WILKENS, H., 527
 WILMOTTE, A., 1166
 WINNEPENNINCKX, B., 641, 1132
 WRIGHT, A-D. G., 285

 XIA, X., 834
Xiphophorus, 1022

 YAMAZAKI, T., 748
 YANG, Z., 451
 yellow, 382
 YOKOYAMA, R., 527
 YOKOYAMA, S., 53, 527
Youngia japonica, 883

Zaprionus, 391
 ZHAO, S., 650
 ZIGLER, JR., J. S., 773
 zoospore fungi, 671
 ZOUIROS, E., 735